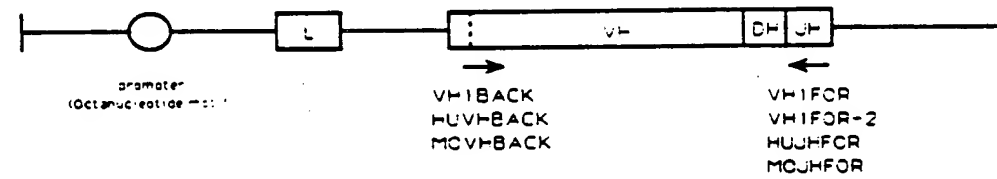
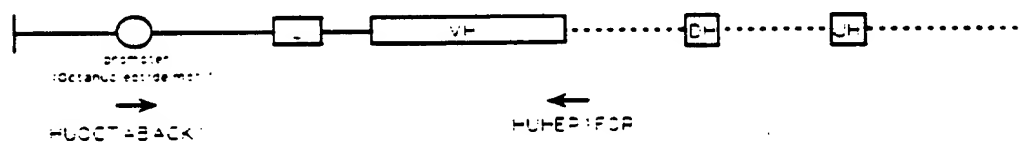


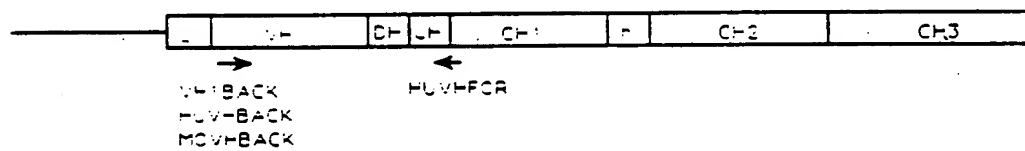
Rearranged heavy chain variable gene (DNA)



Unrearranged heavy chain variable gene (DNA)



Rearranged heavy chain variable gene (mRNA)



Rearranged light chain variable gene (DNA)

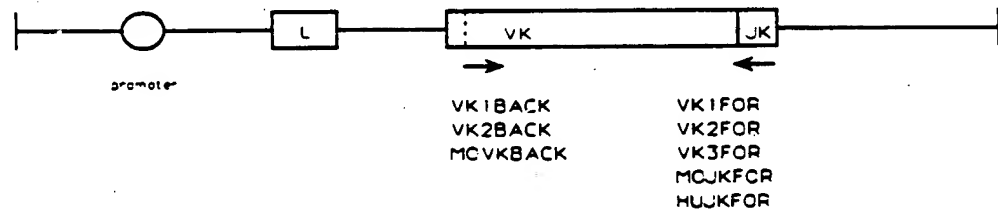


FIG. 1

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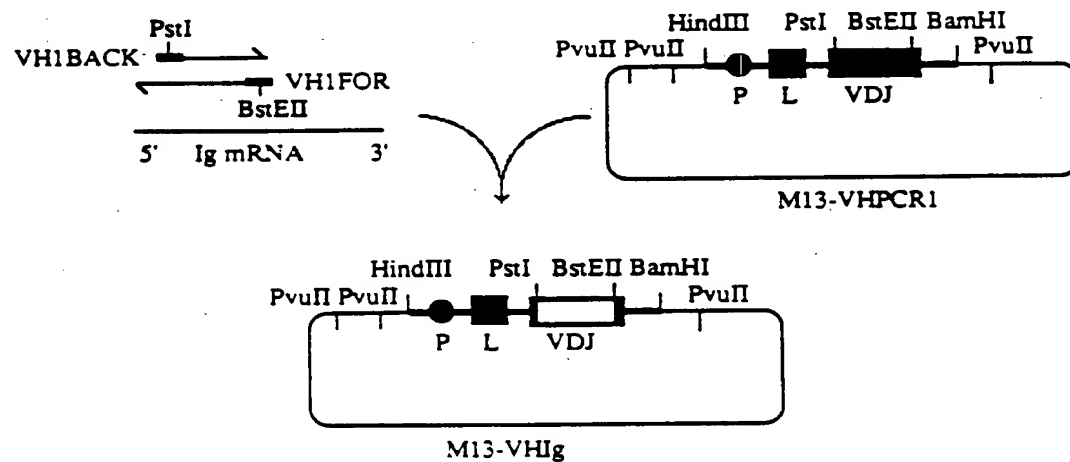


FIG. 2

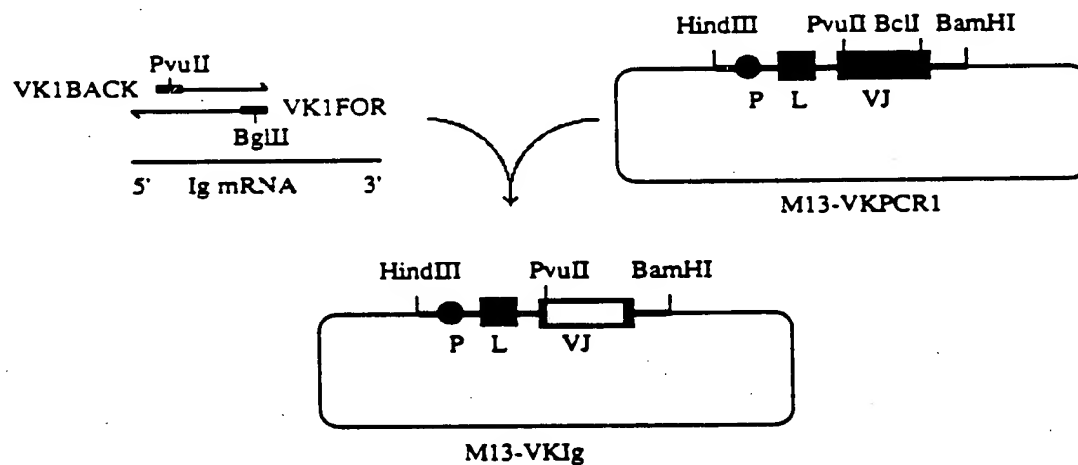


FIG. 4

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M13 VHPCR1

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Hind III

1
AAGCTTATGAATATGCAAAATCTCTGAAATCTACATGGTAAATATAGGTTTGTCTATACCA
10 20 30 40 50 60

CAAACAGAAAAACATGAGATCAGATTCTCTCTACAGTTACTGAGCACACAGGACCTCAC
70 80 90 100 110 120

M G W S C I I L F L V A T A T
CATGGGATGGAGCTGTATCATCTCTCTCTGGTAGCAACAGCTACAGGTAAGGGGCTCAC
130 140 150 160 170 180

AGTAGCAGGCTTGAGGTCTGGACATATATATGGGTGACAAATGACATCCACTTTGCCTTTC
190 200 210 220 230 240

PstI

1 51 10
G V H S Q V Q L Q E S G P G L V R P
TCTCCACAGGTGTCTCACTCTCCAGGTCCTCACTCCAGGAGAGCGGTCCAGGTCTTGTGAGAC
250 260 270 280 290 300

CDR1

15 20 25 30
S Q T L S L T C T V S G S T F S S Y W M
CTAGCCAGACCTTGAGCTCTGAGCTGACCTGACCTGTCTGGCAGCAGCTTCAGGAGCTACTGGA
310 320 330 340 350 360

CDR2

35 40 45 50
H W V R Q P P G R G L E W I G R I D P N
TGCCTGGGTGAGACAGCCACCTGGACAGGTCTTGGTGGATTGGAAGGATTGATCCTA
370 380 390 400 410 420

55 60 65 70
S G G T K Y N E K F K S R V T M L V D T
ATAGTGGTGGTACTAAGTACAATGAGAAGTTCAAGAGCAGAGTGACAATGCTGGTAGACA
430 440 450 460 470 480

75 80 85 90
S K N Q F S L R L S S V T A A D T A V Y
CCAGCAAGAACCAGTTCCAGCTGAGATTAGCAGCGTGACAGCCGCCGACACCCGGCTCT
490 500 510 520 530 540

CDR3

95 100 105 110
Y C A R Y D Y Y G S S Y F D Y W G Q G T
ATTATGTGCAAGATAGGATTACTACGGTAGTAGCTACTTTGACTACTGGGGCCCAAGGGA
550 560 570 580 590 600

BstEII

115 120
T V T V S S
CCACGGTACCTCTCTCTCAGGTGAGTCTTACAACCTCTCTCTTCTATTTCAGCTTAAAT
610 620 630 640 650 660

AGATTTTACTGCAATTTGTTGGGGGGGAAATGTGTGTATCTGAATTTTCAGGTTCATGAAGGA
670 680 690 700 710 720

CTAGGGACACCTTGGGAGTCAGAAAGGCTCATTTGGGAGCCCGGCTGATGCAGACAGACA
730 740 750 760 770 780

BamHI

TCTCAGCTCCAGACTTCATGGCCAGAGATTATAG
790 800 810

FIG. 3

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ML3 V_hPCR1

Hind III

AAGCTTATGAATATGCAAAATCTCTGAACTGATGCTAAATATAGGTTTGTATATACCA
38 48 58 68 78 88

CAAACAGAAAAACATGAGATCACAGTCTCTGTACAGTACTGAGCACACAGGACCTCAC
98 108 118 128 138 148

M G W S C I I L F L V A T A T
CATGGGATGGAGCTGTATCATCTCTCTTGGTAGCAACAGCTACAGGTAAGGGGCTCAC
158 168 178 188 198 208

AGTAGCAGGCTTGAGGCTCTGGACATATATATGGGTGACAATGACATCCACTTTGCCTTTC
218 228 238 248 258 268

Pvu II

G V H S D : C L T Q S P S S L S A S
TCTCCACAGGCTGTCCACTCTGGACATCTGCTGACAGAGCCCAAGCAGCCTGAGCGCCA
278 298 308 318 328

CDR1

15 20 25 30
V G D R V T I T C R A S G N I H N Y L A
GGGTGGGTGACAGAGTGACCATCACCTGTAGAGCCGCGTAACATCCACAAGTACCTGG
338 348 358 368 378 388

CDR2

35 40 45 50
W Y Q Q K P G K A P K L L I Y Y T T T L
CTTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTACTACACCACCCACC
398 408 418 428 438 448

55 60 65 70
A D G V P S R F S G S G S G T D F T F T
TGGCTGACGGGTGTGCCAAGCAGATTACGCGGTAGCGGTACCGTACCGACTTCACCTTCA
458 468 478 488 498 508

CDR3

75 80 85 90
I S S L Q P E D I A T Y Y C O H F W S T
CCATCAGCAGCCTCCAGCCAGAGGACATCGCCACCTACTACTGCCAGCACTTCTGGAGCA
518 528 538 548 558 568

Bcl I (requires dam⁻ host)

95 100 105 108
P R T F G Q G T K V V I K R
CCCCAAGGACGTTTCGGGCAAGGGACCAAGGTGGTGAACCAACGTGAGTAGAATTTAACT
578 588 598 608 618 628

BamHI

TTGCTTCTCTCAGTTGGAATG
638 648

FIG. 5

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Sequence of MB1 VH

Splice -1
↓ G V H S
AGGTGTCCACTCC

1 PstI 10
Q V Q L Q E S G T E L A S P G A S V T L
CAGGTCCCACTCCAGGAGTCAAGAACTGAGCTGGCGAGTCTCTGGGGCATCAGTGACACTG
VH1BACK SITE

30 CDR1 40
S C K A S G Y T F T D H I N W V K K R
TCCTGCAAGGGTCTGGCTACACATTACTGACCATATTATAAATTGGGTAAAAAGAGG
52a 53 CDR2
P G Q G L E W I G R I Y P V S G V T N Y
CCTGGACAGGGGCTTGAGTGGATTGGAAGGATTTATCCAGTAAGTGGTGTAACTAACTAC
60 CDR2 65 70
N K F M G K A T F S V D R S S N T V Y
AATCAAAAATTTCATGGGCAAGGCCACATTCTCTGTAGACCGGTCTCTCAACACAGTGTAC
80 82A B C 83 90 CDR3
M V L N S L T S E D P A V Y Y C G R G F
ATGGTGTGAAACATCTGACATCTGAGGACCTGCTGTCTATTACTGTGGAAGGGGCTT
103 BstEII Splice
D F D V W G Q G T T V T V S S
GATTTTGACTACTGGGGCAAGGGACACGGTCACTCTCTCTCAGG.....
VH1FOR SITE

Sequence of MB1 VK

Splice -1
↓ G V H S
AGGTGTCCACTCC

1 PvuII 10
D I Q L T Q S P P S L T V S V G E R V T
GACATTGAGCTCCAGTCTCTCCATCCCTGACTGTGTCACTAGGAGAGAGGGTCACT
VK1BACK SITE

21A B C D E F CDR1
I S C K S N O N L L W S G N R R Y C L G
ATCAGTTGCAAAATCCAATCAGAATCTTTATGGAGTGGAAACCGAAGGTACTGTTTGGGC
35 40 50 CDR2
W H Q W K P G Q T P T P L I T W T S D R
TGGCACCAGTGGAAACCAAGGGCAAACTCCTACACCGTTGATCACCTGGACATCTGATAGG
60 70
F S G V P D R F I G S G S V T D F T L T
TTCTCTGGAGTCCCTGATCGTTTCATAGGCAGTGGATCTGTGACAGATTTCCTCTGACC
80 90 CDR3
I S S V Q A E D V A V Y F C Q Q H L D L
ATCAGCAGTGTGCAGGCTGAAGATGTGGCAGTTTATTCTGTGACCAACATTGACCTT
95 100 BglII/BclI Splice
P Y T F G G G T K L E I K
CCGTACAGTTCGGAGGGGGGACCAAGCTGGAGATCAAACGTGAG
VK1FOR SITE

FIG. 6

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α -Lys 30

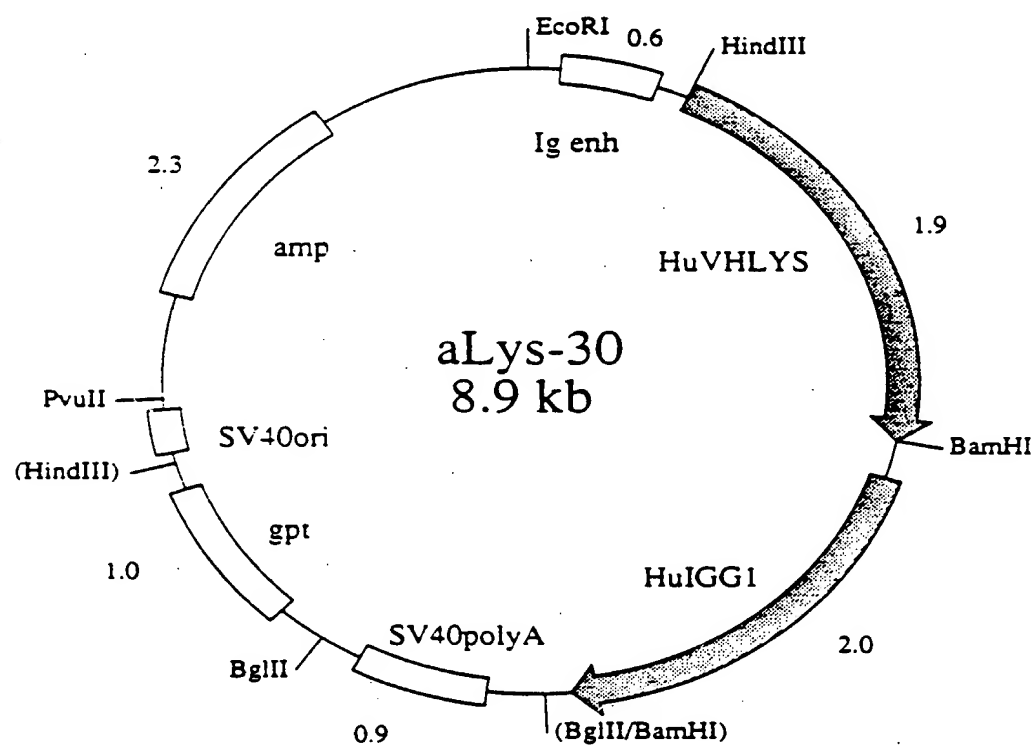


FIG. 7

α -Lys 17

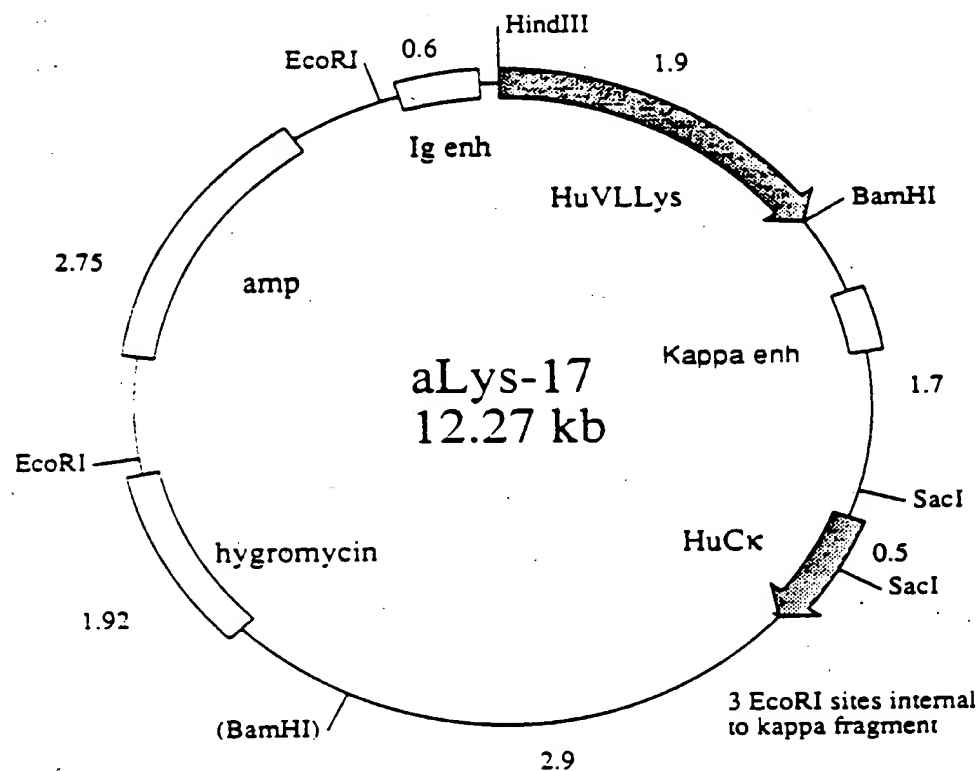


FIG. 8

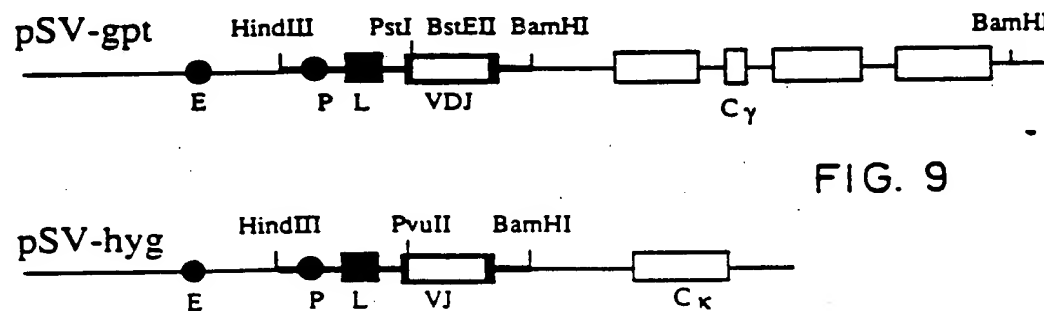


FIG. 9

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ER1

CDR1

ER2

CDR2

KABAT 1A

AC7	PGLVQPSQSLSTTCSTVQYSLT	SGYYW	WRCPPGKLEWLG	YISYDGSNNYNPSLKN
AC9	PGLVQPSQSLSTTCSTVQYSLT	SGYYW	WRCPPGKLEWLG	YITHSGSTTYNPSLQS
EC3	PGLVQPSQSLSTTCSTVQYSLT	SGYYW	WRCPPGKLEWLG	YISYDGSNNYNPSLKN
GC1	PGLVQPSQSLSTTCSTVQYSLT	SGYYW	WRCPPGKLEWLG	YISYDGSNNYNPSLKN

KABAT 1B

AC6	PVLVAPPSQSLSTTCVSGFSLT	NYGVL	WRCPPGKLEWLG	VTHAGGSTNYNSALMS
25G07	PGLVQPSQSLSTTCVSGFSLT	SYGVL	WRCPPGKLEWLG	VTHSGGSTDYNAAFIS
BC3	PGLVAPPSQSLSTTCVSGFSLT	SYGVL	WRCPPGKLEWLG	VTHSGGSTNYNSALMS
GC3	PGLVQPSQSLSTTCVSGFSLT	SYGVL	WRCPPGKLEWLG	VTHSGGSTDYNAAFIS
H09	PVLVAPPSQSLSTTCVSGFSLT	SYGVL	WRCPPGKLEWLG	VTHAGGSTNYNSALMS
25G10	PGLVAPPSQSLSTTCVSGFSLT	SYGVL	WRCPPGKLEWLG	VTHSGGSTNYNSALMS
AL2	PGLVAPPSQSLSTTCVSGFSLT	SYGVL	WRCPPGKLEWLG	VTHSGGSTNYNSALMS
AC8	PGLVAPPSQSLSTTCVSGFSLT	SYGVL	WRCPPGKLEWLG	VTHSGGSTNYNSALMS
25G08	PGLVAPPSQSLSTTCVSGFSLT	SYGVL	WRCPPGKLEWLG	VTHSGGSTNYNSALMS
AC3	PGLVQPSQSLSTTCVSGFSLT	SYGVL	WRCPPGKLEWLG	VTHSGGSTDYNAAFIS
CC7	PVLVAPPSQSLSTTCVSGFSLT	SYGVL	WRCPPGKLEWLG	VTHAGGSTNYNSALMS
H04	PGLVAPPSQSLSTTCVSGFSLT	SYGVL	WRCPPGKLEWLG	VTHSGGSTNYNSALMS

KABAT 11A

EC1	PELLVPPGVSXKLSCHSGSYTFT	DYAMH	WRCPPGKLEWLG	VISTYYGDSYNNQKFKG
H07	PELLVPPGVSXKLSCHSGSYTFT	DYAMH	WRCPPGKLEWLG	VISTYYGDSYNNQKFKG

KABAT 11B

AC1	AEILVPPGASVXLSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
BC4	AEILVPPGASVXMSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIVPGSGSTNYNEKFKS
CC3	AEILVPPGASVXLSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
CC9	AEILVPPGASVXLSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
CC6	AEILVPPGASVXMSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
CC8	AEILVPPGASVXLSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
EC7	AEILVPPGASVXLSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
GC8	AEILVPPGASVXLSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
GC1	AEILVPPGASVXMSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
25G09	AEILVPPGASVXMSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
FC4	AEILVPPGASVXLSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
H04	AEILVPPGASVXLSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
H01	AEILVPPGASVXLSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
25G05	AEILVPPGASVXMSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
BC1	AEILVPPGASVXMSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
BC3	AEILVPPGASVXMSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
BC1	AEILVPPGASVXMSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG

KABAT 111 A

25G03	GGILVPPGGSLSLSCAASGFTTF	DYAMS	WRCPPGKLEWLG	FIRNKANGYTTEYSASVKG
CC1	GGILVPPGGSLSLSCAASGFTTF	DYAMS	WRCPPGKLEWLG	FIRNKANGYTTEYSASVKG
BC7	GGILVPPGGSLSLSCAASGFTTF	DYAMS	WRCPPGKLEWLG	FIRNKANGYTTEYSASVKG

KABAT 111 B

GC1	GGILVPPGGSLSLSCAASGFTTF	DYAMS	WRCPPGKLEWLG	YISSGGSTYYADTVKG
BC2	GGILVPPGGSLSLSCEASNEYEFF	SHDMS	WRCPPGKLEWLG	AINDSGGSTYYPDTHF
CC4	GGILVPPGGSLSLSCAASGFTTF	SYAMS	WRCPPGKLEWLG	AISGSGGSTYYADSVKG
CC3	GGILVPPGGSLSLSCAASGFTTF	SYAMS	WRCPPGKLEWLG	AISGSGGSTYYADSVKG
FC2	GGILVPPGGSLSLSCEASNEYEFF	SHDMS	WRCPPGKLEWLG	AINDSGGSTYYPDTHF
FC6	GGILVPPGGSLSLSCAASGFTTF	SYAMS	WRCPPGKLEWLG	AISGSGGSTYYADSVKG
CC2	GGILVPPGGSLSLSCEASNEYEFF	SHDMS	WRCPPGKLEWLG	AINDSGGSTYYPDTHF
FC9	GGILVPPGGSLSLSCAASGFTTF	SYAMS	WRCPPGKLEWLG	YISSGGSTYYADSVKG

KABAT 111 C

EC6	GGILVPPGGSLSLSCAASGFTTF	DYAMS	WRCPPGKLEWLG	FIRNKANGYTTEYSASVKG
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KABAT V A

CC4	AEILVPPGASVXLSCHASGYTFT	SYAMH	WRCPPGKLEWLG	EIDPDSGYTNYNNQKFKG
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FIG. 10a

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CDR 2

FRAMWORK 3

CDR 3

KABAT HUMAN VH1

	STSTAYMELSLRSEDVAVYYCAR	GEGWQHFDY
HACKFQG	RVTIRRHKSTSTAYMELSSLRSEDVAVYYCAR	GSRYGYDCSGYYL
GYACKFQG	RVTMTNRTSISTATMELSSLRSEDVAVYYCAR	LAHFGSPVDWFDP

KABAT HUMAN VH2

KHQLQPSLKS	RVTISVDTSKNQFSLKLSVTAADTAVYYCAR	GGVVPAAIMDV
KS	RVTISVDTSKNQFSLKLSVTAADTAVYYCAR	MARYYDFWSGYSAYYDY
SLKS	RLSISGQTSRNQFSLKLSVTAADTAVYYCAR	HRNWGSPVHFQY
	ESTSTAYMELSSLRSEDVAVYYCAR	DSYGQYGGHY

KABAT HUMAN VH3

ISYITSSSSYTNVADSVKG	RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR	DGRFGTYSPSDY
SVKG	RFTISRDDSKSIAYLQVNSLKTEDTAVYYCTR	TIYYDSSGYPYW
YADSVKG	RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR	GIALDAFDI
YYADSVRO	RFTISRDNKNTLYLQMNSLRAEDTAVYYCAR	53 NT. UNPROD REARR
DSVKG	RFTISRDNKNSLYLQMNSLRDEDTAVYYCAR	DHSGTGCGGSGSYF
VSAISGSGGSTYYADSVKG	RFTISRDNKNTLYLQMNSLRSEDVAVYYCAR	KDNLWFDP
AVISYDGSNKYYADSVKG	RFTISRDNKNTLYLQMNSLRAEDTAVYYCAR	DLGGRGVVVVPAPGGRSIIYYGMDV
GAVISYDGSNKYYADSVKG	RFTISRDNKNTLYLQMNSLRAEDTAVYYCAR	LEGIGTIYYYGMDV
	AKNSLYLQMNSLRAEDTAVYYCVR	DDSSSWPKHFQH
QYAASVKG	RFTISRDDSKNSLYLQMNSLNTEDTAVYYCVR	SGVVPYLDY

KNOWN FAMILY

AVYYCAR	DPRIAARPDYYYYMDV
TAMYYCAR	GAEVVEPTARYYYGLNV

FIG. 11

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FR1	CDR1	FR2
YTTT	SYGIS	WVTTGPWTRLLRWMG
GEKPGSSVKV/SCKASGYTFT	DYFMN	WMRQAPGQRLWWMG
QVQLQEIIGPRTGEASETSLSLICAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
QVQLQESGPGLVK*SETLSLTCTVSGGSIS	SYIWS	WIRQPPGKGLEWIG
GYTFT	NYCMH	WVRQDHAQGLEWIG
QVQLQESGPGLVKpSETLSLYCAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
GPRLGEASETSLSLTCTVSGGSIS	SSSYW	WIRQPPGKGLEWIG
QVQLQESGPGLVKpSETLSLTCTVSGGSIS	SYIWS	WIRQPPGKGLEWIG
LSLICAVSGGSIS	SGNW*1	WVRQPPGKGLEWIG
SETLSLTCAVYGGSF	GYIWS	WIRQPPGKGLEWIG
QVQLVQSGAEVKKPGASVK/SCKASGYTFT	NYCMH	WVRQVLAQGLEWIG
SETLSLICAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
SRAQTGEASETSLSLTCTVSGGSIS	SSSYWG	WIRQPPGKGLEWIG
CPLTCTVSGGSVSSGS	YIWS	WIRQPPGKGLEWIG
GLVKPSETLSLTCTVSGGSIS	SYIWS	WIGSPGKGLEWIG
SFETLSLICAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
QVQLVQSGAEVKKPGSSVK/SCKASGDTT	SYAIS	WVRQAPGQGLEWIG
QVQLQGWGAGLLKPSSETLSLTCAVYGGSF	GYIWS	WIRQPPGKGLEWIG
QVQLQESGPGLVKpSETLSLTCTVSGGSIS	SSSYWG	WIRQPPGKGLEWIG
GPGLVKPSQTLSLTCTVSGGSIS	SGGYWS	WIRQNPgKGLEWIG

* indicates stop codon (unsure as sequence remains in frame)
• sequence terminates due to internal restriction site
lower case denotes frame shift

CDR1	FR1	CDR3
WISAYNGNTNYAQKLCG	RVTITDTSSTAYMELSLRSDDTAVYYCAR	DTVSS
WINAGNGNTKYSQKLCG	RVTITRDTASTAYMQLSSLRSEDATAVYYCAR	DTVSS
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS*	
RIYTSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	DTVSS
LVCPSDGSSTAYAQKFA	RVTITRDTSMSTAYMELSSLRSEDATAVYYCAR	DTVSS
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS*	
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSS*	
YIYSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSS*	
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS*	
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	DTVSS
LVCPSDGSSTAYAQKFA	RVTITRDTSMSTAYMELSSLRSEDATAVYYCAR	DTVSS
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS*	
SIYSGSTYYNPSLKS	RVTIPVDTSKNQFSLKLSS*	
YIYSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	DTVSS
RIYTSGSTNYNPSLKS	RVTMSVDTSKNQFSLKLSS*	
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLS*	
RIIPILGIANAYAQKFG	RVTITADKSTAYMELSSLRSEDATAVYYCAR	DTVS
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSS*	
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLSS*	
YIYSGSTYYNPSLKS	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	DTVSS

FIG. 12

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psw.

HindIII site AAGCTT

GCATGCAAAATTTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCGGTACGGCAGCC
10 20 30 40 50 60

M K Y L L P T A A
A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTTATTACTCGCTGCGCCCAACCAGCGATGGCCAGGTGCAGGTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACGTGGCGTGGTGGCGCGCTCACAGAGCGGTGTCCATCAGTGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGCGCTATGGTGTAAACTGGGTTCGCCAGCGCTCCAGGAAAGGTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTTGGGGTGTATGGAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACTCCAAAGAGCCAAAGTTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S SmaI
CAAGGCACCACGGTCACCGTCTCTCTCATAATAAGAGCTATCTGGGGCTAAGCTCGAATTC
430 440 450 460 470 480

FIG. 13

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PSW2

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HindIII AAGCTT

GCATGCAAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGGCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCCCAACCAGCGATGGCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCCTGGTGGCGCCCTCACAGCGCTGTTCATCATATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAAACCGGCTATGGTGTAAACTGGGTTGGCCAGCTCCAGGAAAGGGTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTGGGGTGATGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACCTCCAAAGAGCCCAAGTTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S
CAAGGCACCAAGGCTCAGCTCTCTCTCATAATAAGAGCTCGAATTCGCCAAGCTTGCATGC
430 440 450 460 470 480

A A T T C T A T T T C A A G G A G A C A G T C A T A T G A A A T A C C T A T T G C C T A C G G C A G C C G C T G G A
490 500 510 520 530 540

L L L L A A Q P A M A D I V L T Q S P A
TTGTTATTACTCGCTGCCCCAACCAGCGATGGCCGACATCGTCTGACTCAGTCTCCAGCC
550 560 570 580 590 600

S L S A S V G E T V T I T C R A S G N I
TCCCTTTCTGCGTCTGTGGGAGAACTGTCCACCATCACATGTCGAGCAAGTGGGAATATT
610 620 630 640 650 660

H N Y L A W Y Q Q K Q G K S P Q L L V Y
CACAATTATTTAGCATGGTATCGAGAGAAACAGGAAAAATCTCTCAGCTCTCTGGTCTAT
670 680 690 700 710 720

FIG. 14a

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Y T T T L A D G V P S R F S G S G S G T
TATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTGAGTGGCAGTGGATCAGGAACA
730 740 750 760 770 780

Q Y S L K I N S L Q P E D F G S Y Y C Q
CAATATTCTCTCAAGATCAACAGCCTGCAACCTGAAGATTTTGGGAGTTATTACTGTCAA
790 800 810 820 830 840

H F W S T P R T F G G G T K L E I K R
CATTTTGGAGTACTCCTCGGACGTTGCGTGGAGGCACCAAGCTGGAAATCAAACGGTAA
850 860 870 880 890 900

TAAGAGCTCGAATTC
910

FIG. 14 b

pSWLHPOLYMYC
HindIII site AAGCTT

M K Y L L P T A A
GCATGCAAAATTCATTTCAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAG
70 80 90 100 110 PstI

Polylinker
TCTAGA GTCGAC CTCGAG
XbaI SalI XhoI

MYC PEPTIDE
V T V S S E O K L I S E E D L N * *
GGTCACCGTCTCCTCAGAACAAAACTCATCTCAGAAGAGGATCTGAATTAATAA
BstEII

GGGCTAAGCTCGAATTC

FIG. 15

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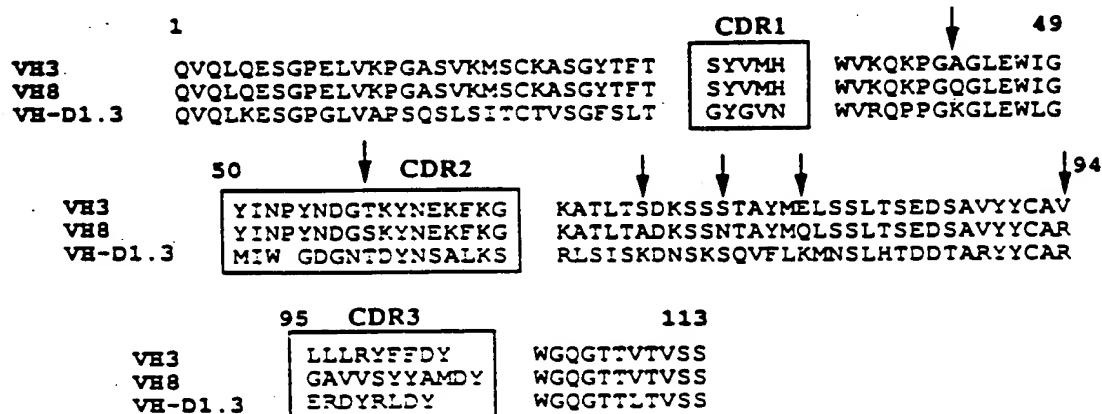


FIG. 16

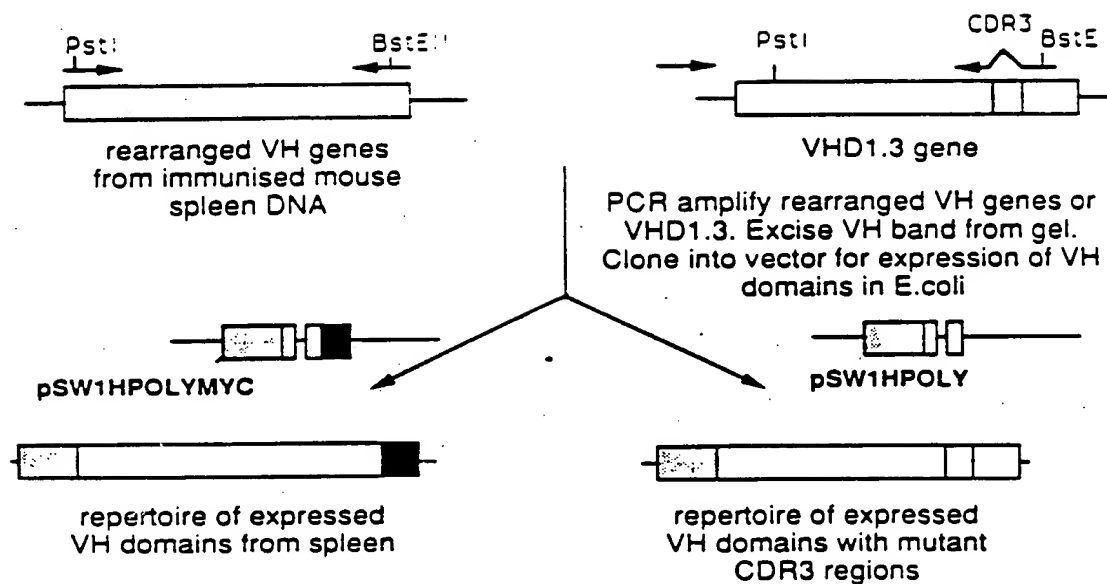


FIG. 17

NO ATTITUDE CHART

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Assay for binding to antigen

FIG. 18

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pSW2HPCLY

HindIII AAGCTT

GCATGCAAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCGCTACGGCAGCC
10 20 30 40 50 60

AGLLLLAQAQVQLQ
GCTGGATTGTTATTACTGCGCTGCCCAACCAGCGATGGCCAGGTGCAGCTGCAG
70 80 90 100 110 PstI

TCTAGA GTCGAC CTCGAG
XbaI SalI XhoI

VTVS
GGTCACCCTCTCTCTCATAATAAGAGCTCGAATTCGCCAAGCTTGCATGC
EcoRII 430 440 450 460 470 480

AAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCGCTACGGCAGCCGCTGGA
490 500 510 520 530 540

LLLLAQAQADIVLTQSPA
TTGTTATTACTGCGCTGCCCAACCAGCGATGGCCAGCATCGTCTGACTCAGTCTCCAGCC
550 560 570 580 590 600

SLSA SVGETVTITCRASGN
TCCCTTTCTGCGCTCTGTGGGAGAACTGTCCAGCATCAGTGTGAGCAAGTGGGAATATT
610 620 630 640 650 660

HNYLAWYQQQKQGSFPQLLVY
CACCAATTATTTAGCATGGTATCAGCAGAAACAGGGGAAATCTCTCAGCTCCTGGTCTAT
670 680 690 700 710 720

YTTTLADGVPSRFSGSGSGT
TATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTCAAGTGGCAGTGGATCAGGAACA
730 740 750 760 770 780

QYSLKINS LQPEDFGSYYCQ
CAATATTCTCTCAAGATCAACAGCGCTGCAACCTGAAGATTTGGGAGTTATTACTGTCAA
790 800 810 820 830 840

HFWSTPRTFGGGTKLEIKR
CATTTTGGAGTACTCTCTCGGACGTTGCGGTGGAGGCACCAAGCTGGAAATCAAACGGTAA
850 860 870 880 890 900

TAAGAGCTCGAATTC
910

FIG. 19

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M K Y L L P T
AAGCTTGCATGCAAATTCATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACG
10 20 30 40 50 60
A A A G L L L L A A Q P A M A Q V Q L Q
GCAGCCGCTGGATTGTTTACTCGCTGCCCAACCAGCGATGGCCCGAGGTGCAGCTGCAG
70 80 90 100 110 120
E S G P G L V A P S Q S L S I T C T V S
GAGTCAGGACCTGGCGCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCA
130 140 150 160 170 180
G F S L T G Y G V N W V R Q P P G K G L
GGGTTCTCATTAAACCGCTATGGTGTAAACTGGGTTGCCAGCCTCCAGGAAAGGGTCTG
190 200 210 220 230 240
E W L G M I W G D G N T D Y N S A L K S
GAGTGGCTGGGAATGATTGGGGTGATGGAAACACAGACTATAATTGAGCTCTCAAATCC
250 260 270 280 290 300
R L S I S K D N S K S Q V F L K M N S L
AGACTGACATCAGCAAGGACAACTCCAAGAGCCAGTTTCTTAAAAATGAACAGTCTG
310 320 330 340 350 360
H T D D T A R Y Y C A R E R D Y R L D Y
CACACTGATGACACAGCCAGGTACTACTGTCCAGAGAGAGAGATTATAGGCTTGACTAC
370 380 390 400 410 420
W G Q G T T V T V S S G G G A P A A A P
TGGGGCCAAAGGCACCAAGGTGACCGTCTCTCAGGTGGTGGTGGTCCAGCAGCTGCACCT
430 440 450 460 470 480
A G S G C V Q L K E S G P G L V A P S Q
GCTGGAGGAGGACAGGTGCAGCTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAG
490 500 510 520 530 540
S L S I T C T V S G F S L T G Y G V N W
AGCCTGTCCATCACATGCACCGTCCAGGGTTCTCATTAAACCGGCTATGGTGTAAACTGG
550 560 570 580 590 600
V R Q P F G K G L E W L G M I W G D G N
GTTGCCAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAATGATTGGGGTGATGGAAAC
610 620 630 640 650 660
T D Y N S A L K S R L S I S K D N S K S
ACAGACTATAATTGAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACTCCAAGAGC
670 680 690 700 710 720
Q V F L K M N S L H T D D T A R Y Y C A
CAAGTTTCTTAAAAATGAACAGTCTGCACACTGATGACACAGCCAGGTACTACTGTGCC
730 740 750 760 770 780
R E R D Y R L D Y W G Q G T T V T V S S
AGAGAGAGAGATTATAGGCTTGACTACTGGGGCCAAAGGCACCAAGGTGACCGTCTCTCA
790 800 810 820 830 840
TAATAAGAGCTC
850

FIG. 20

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M K Y L L P T A A

GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGGCTATGGTGTAACTGGGTTGCCAGCCTCCAGGAAAGGGTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTGGGGTGATGGAACACAGACTATAATTCAGCTCTCAAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACTCCAGAGCCAGTTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S R T P E M P V L E N R
CAAGGCACCCAGGTACCGTCTCCTCACGGACACCAGAAATGCCTGTTCTGGAAAACCGG
430 440 450 460 470 480

A A Q G D I T A P G G A R R L T G D Q T
GCTGCTCAGGGCGATATTACTGCACCCGGCGGTGCTCGCCGTTTAAACGGGTGATCAGACT
490 500 510 520 530 540

A A L R D S L S D K P A K N I I L L I G
GCCGCTCTGCGTATTCTCTTAGCGATAAACCTGCAAAAAATATTATTTTGCTGATTGGC
550 560 570 580 590 600

D G M G D S E I T A A R N Y A E G A G G
GATGGGATGGGGGACTCGGAAATTACTGCCGCACGTAATTATGCCGAAGGTGCGGGCGGC
610 620 630 640 650 660

F F K G I D A L P L T G Q Y T H Y A L N
TTTTTAAAGGTATAGATGCCTTACCGCTTACCGGGCAATACACTCACTATGCGCTGAAT
670 680 690 700 710 720

K K T G K P D Y V T D S A A S A T A W S
AAAAAACCGGCAACCGGACTACGTACCGACTCGGCTGCATCAGCAACCGCTGGTCA
730 740 750 760 770 780

FIG. 21a

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T G V K T Y N G A L G V D I H E K D H P
ACCGGTGTCAAAACCTATAACGGCGCGCTGGGGCTCGATATTCACGAAAAAGATCACCCA
790 800 810 820 830 840

T I L E M A K A A G L A T G N V S T A E
ACGATTCTGGAAATGGCAAAAGCCGAGGTCTGGCGACCGGTAACGTTTCTACCGCAGAG
850 860 870 880 890 900

L Q D A T P A A L V A H V T S R K C Y G
TTGCAGGATGCCACGCCCGCTGCGCTGGTGGCACATGTGACCTCGCGCAAATGCTACGGT
910 920 930 940 950 960

P S A T S E K C P G N A L E K G G K G S
CCGAGCGCGACCAAGTGAATAATGTCCGGGTAACGCTCTGGAAAAAGGCGGAAAGGATCG
970 980 990 1000 1010 1020

I T E Q L L N A R A D V T L G G G A K T
ATTACCGAACAGCTGTTAACGCTGCTGCCGACGTTACGCTTGGCGGGCGGCGCAAAACC
1030 1040 1050 1060 1070 1080

F A E T A T A G E W Q G K T L R E Q A Q
TTTGCTGAAACGGCAACCGCTGGTGAATGGCAGGGAAAAACGCTGCGTGAACAGGCACAG
1090 1100 1110 1120 1130 1140

A R G Y Q L V S D A A S L N S V T E A N
GCGCGTGGTTATCAGTTGGTGAGCGATGCTGCCTCACTGAATTCGGTGACGGAAGCGAAT
1150 1160 1170 1180 1190 1200

Q Q K P L L G L F A D G N M P V R W L G
CAGCAAAAACCCCTGCTTGGCCTGTTGCTGACGGCAATATGCCAGTGCGCTGGCTAGGA
1210 1220 1230 1240 1250 1260

P K A T Y H G N I D K P A V T C T P N P
CCGAAAGCAACGTACCATGGCAATATCGATAAGCCCGCAGTCACCTGTACGCCAAATCCG
1270 1280 1290 1300 1310 1320

Q R N D S V P T L A Q M T D K A I E L L
CAACGTAATGACAGTGATACCAACCCCTGGCGCAGATGACCGACAAAGCCATTGAATTGTTG
1330 1340 1350 1360 1370 1380

S K N E K G F F L Q V E G A S I D K Q D
AGTAAAAATGAGAAAGGCTTTTCTCTGCAAGTTGAAGGTGCGTCAATCGATAAACAGGAT
1390 1400 1410 1420 1430 1440

H A A N P C G Q I G E T V D L D E A V Q
CATGCTGCGAATCCTTGTGGGCAAATGGCGAGACGGTCGATCTCGATGAAGCCGTACAA
1450 1460 1470 1480 1490 1500

P A L E F A K K E G N T L V I V T A D H
CGGGCGCTGGAATTCGCTAAAAAGGAGGGTAACACGCTGGTCATAGTCACCGCTGATCAC
1510 1520 1530 1540 1550 1560

FIG. 21b

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A H A S Q I V A P D T K A P G L T Q A L
G C C C A C G C C A G C C A G A T T G T T G C G C C G G A T A C C A A G C T C C G G G C C T C A C C C A G G C G C T A
1570 1580 1590 1600 1610 1620

N T K D G A V M V M S Y G N S E E D S Q
A A T A C C A A A G A T G G C G C A G T G A T G G T G A T G A G T T A C G G G A A C T C C G A A G A G G A T T C A C A A
1630 1640 1650 1660 1670 1680

E H T G S Q L R I A A Y G P H A A N V V
G A A C A T A C C G G C A G T C A G T T G C G T A T T G C G G C G T A T G G C C C G C A T G C C G C C A A T G T T G T T
1690 1700 1710 1720 1730 1740

G L T D Q T D L F Y T M K A A L G L K *
G G A C T G A C C G A C C A G A C C G A T C T C T T C T A C A C C A T G A A A G C C G C T C T G G G G C T G A A A T A A
1750 1760 1770 1780 1790 1800

A A C C G C G C C C G G A G T G A A T T T T C G C T G C C G G T G G T T T T T T T G C T G T T A G C
1810 1820 1830 1840 1850

FIG. 21c

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GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

M K Y L L P T A A
A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGGCTATGGTGTAAGTGGGTTCCGCCAGCCTCCAGGAAAGGTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTGGGGTGATGGAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAAGTCCAAGAGCCAAGTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S * *
CAAGGCACCACGGTCACCGTCTCCTCATAATAAGAGCTATCCCGGGAGCTTGCATGCAAA
430 440 450 460 470 480

M K Y L L P T A A A G L
TTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTG
490 500 510 520 530 540

L L L A A Q P A M A D I E L V D L E I K
TTATTACTCGCTGCCCAACCAGCGATGGCCGACATCGAGCTCGTCGACCTCGAGATCAAA
550 560 570 580 590 600

R E Q K L I S E E D L N * *
CGGGAACAAAACCTCATCTCAGAAGAGGATCTGAATTAATAATGATCAAACGGTAATAAG
610 620 630 640 650 660

GATCCAGCTCGAATTC
670

FIG. 22

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Q V Q L Q E S G P G L V Q P S Q S L S I
CAGGTGCAGCTGCAGGAGTCAGGACCTGGCCTAGTGCAGCCCTCAGAGCCTGTCCATC
10 20 30 40 50 60

T C T V S G F S L T S Y G V H W V R Q S
ACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTCCGCCAGTCT
70 80 90 100 110 120

P G K G L E W L G M I W G D G N T D Y N
CCAGGAAAGGGTCTGGAGTGGCTGGGAATGATTGGGGTGATGGAAACACAGACTATAAT
130 140 150 160 170 180

S A L K S R L S I S K D N S K S Q V F L
TCAGCTCTCAATCCAGACTGAGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTCTTA
190 200 210 220 230 240

K M N S L H T D D T A R Y Y C A R E R D
AAAATGAACAGTCTTGCACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGAT
250 260 270 280 290 300

Y R L D Y W G Q G T T V T V S S
TATAGGCTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCTCA
310 320 330 340

FIG. 23

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